

IN THE CLAIMS

1. (currently amended) An *in vitro* ~~A~~ method of diagnosing non-small cell lung cancer (NSCLC) in a human, the method comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human obtained from a bronchial lavage, whereby a lower degree of expression of the gene in the human relative to a normal level of expression of the gene in humans not afflicted with NSCLC is an indication that the human is afflicted with NSCLC.

2-44. (canceled)

45. (currently amended) The method of claim 1 ~~43~~ wherein the cells are epithelial cells.

46. (previously presented) The method of claim 1 wherein the human does not exhibit a macroscopic clinical symptom of NSCLC.

47. (previously presented) The method of claim 46 wherein the symptom is selected from the group consisting of (a) a persistent cough which gets worse over time, (b) constant chest pain, (c) expectoration of blood, (d) shortness of breath, (e) wheezing, (f) hoarseness, (g) recurrent pneumonia, (h) recurrent bronchitis, (i) swelling of the neck and face, (j) loss of appetite, (k) weight loss, and (l) fatigue.

48. (previously presented) The method of claim 1 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

49. (canceled)

50. (previously presented) The method of claim 48 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

51. (previously presented) The method of claim 50 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

52. (previously presented) A method of assessing NSCLC tumorigenesis at an early stage in a human comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, whereby a lower degree of expression of the gene is an indication of early-stage tumorigenesis.

53. (currently amended) A method of selecting a method of treating an NSCLC tumor in a human, comprising steps of:

assessing aggressiveness of the * NSCLC tumor in the * human, comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, whereby a lower degree of expression of the gene is an indication that the tumor is aggressive; and

selecting among methods of treating the NSCLC tumor, wherein a more aggressive treatment is selected if a lower degree of expression is detected.

54. (previously presented) The method of claim 53 wherein the tumor is a diagnostic stage I NSCLC tumor.

55. (canceled)

56. (previously presented) A method of assessing the risk that a human will develop NSCLC comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, wherein a lower degree of expression of the gene in the human relative to a normal level

of expression of the gene in humans not afflicted with NSCLC is an indication that the human is at an increased risk for developing NSCLC.

57. (canceled)

58. (previously presented) The method of claim 52 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

59. (previously presented) The method of claim 58 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

60. (previously presented) The method of claim 59 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

61. (previously presented) The method of claim 53 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

62. (previously presented) The method of claim 61 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

63. (previously presented) The method of claim 62 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

64. (previously presented) The method of claim 56 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

65. (previously presented) The method of claim 64 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

66. (previously presented) The method of claim 65 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.